

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

Claims 1-12. (Cancelled)

Claim 13. (Currently amended) A method for predicting phenotypic resistance of Human Deficiency Virus (HIV) ~~human deficiency virus type 1 (HIV-1)~~ to a therapeutic agent comprising:

(a) providing a neural network;

(b) training a neural network on a training data set, wherein each member of the training data set corresponds to a genetic mutation that correlates to a phenotypic ~~change that causes a change in therapeutic~~ resistance of HIV[[HIV-1]], said training being performed by

- i) propagating a training data set in a feed-forward fashion,
- ii) calculating the associated error,
- iii) back propagating the error,
- iv) adjusting the weights in the neural network,
- v) minimizing the error function by repeating the steps i), ii), iii), iv),
- vi) inputting a testing data set to ensure proper training, said testing data

set comprising members that correspond to at least one genetic mutation, the presence of which correlates to a phenotypic ~~change that cause a change in~~ resistance of HIV[[HIV-1]] to at least one therapeutic agent, which testing data set is different from the training data set:

(c) providing a determined HIV[[HIV-1]] genetic sequence from a patient by

- i) obtaining an HIV[[HIV-1]] sample from the patient,
- ii) obtaining the genetic sequence from the HIV[[HIV-1]] sample; and

d) predicting the phenotypic resistance of HIV[[HIV-1]] to the therapeutic agent by inputting the determined genetic sequence into the trained neural network which computes the predicted phenotypic resistance of HIV[[HIV-1]] to a therapeutic agent, wherein the phenotypic resistance is expressed as the fold-change in the IC₅₀ or IC₉₀ values of one or more therapeutic agents.

Claims 14-17. (Cancelled)

Claim 18. (Original) The method of claim 13, wherein the neural network is a three-layer feed-forward neural network.

Claim 19. (Original) The method of claim 18, wherein the three-layer feed forward network comprises:

- (a) a set of input nodes, wherein each member of the set of input nodes corresponds to a mutation in the genome of the pathogen;
- (b) a plurality of hidden nodes; and
- (c) a set of output nodes, wherein each member of the set of output nodes corresponds to a therapeutic agent used to treat the pathogen.

Claims 20-29. (Cancelled)